



SEQUENCE LISTING

Lehmann, Martin
Lassen, Soren F

<120> Improved Phytases

<130> 5808.200-US

<160> 98

<170> PatentIn version 3.2

<210> 1

<211> 440

<212> PRT

<213> Aspergillus terreus 9A-1

<400> 1

Lys His Ser Asp Cys Asn Ser Val Asp His Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
20 25 30

Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Glu Asp Cys His Ile Thr
35 40 45

Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr His Ser
50 55 60

Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Ser Ala
65 70 75 80

Thr Ala Phe Pro Gly Lys Tyr Ala Phe Leu Gln Ser Tyr Asn Tyr Ser
85 90 95

Leu Asp Ser Glu Glu Leu Thr Pro Phe Gly Arg Asn Gln Leu Arg Asp
100 105 110

Leu Gly Ala Gln Phe Tyr Glu Arg Tyr Asn Ala Leu Thr Arg His Ile
115 120 125

Asn Pro Phe Val Arg Ala Thr Asp Ala Ser Arg Val His Glu Ser Ala
130 135 140

Glu Lys Phe Val Glu Gly Phe Gln Thr Ala Arg Gln Asp Asp His His

RECEIVED

JAN 23 2003

TECH CENTER 1600/2900

145	150	155	160
Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Ala Ile Pro Glu	165	170	175
Gly Ser Ala Tyr Asn Asn Thr Leu Glu His Ser Leu Cys Thr Ala Phe	180	185	190
Glu Ser Ser Thr Val Gly Asp Asp Ala Val Ala Asn Phe Thr Ala Val	195	200	205
Phe Ala Pro Ala Ile Ala Gln Arg Leu Glu Ala Asp Leu Pro Gly Val	210	215	220
Gln Leu Ser Thr Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe	225	230	235
Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys	245	250	255
Asp Leu Phe Thr Ala Thr Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser	260	265	270
Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val	275	280	285
Gln Gly Val Gly Trp Ala Asn Glu Leu Met Ala Arg Leu Thr Arg Ala	290	295	300
Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Ser Pro	305	310	315
Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp	325	330	335
Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr	340	345	350
Ala Pro Leu Ser Gln Thr Ser Val Glu Ser Val Ser Gln Thr Asp Gly	355	360	365
Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu	370	375	380

Met Met Gln Cys Arg Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Met Pro Leu His Gly Cys Pro Thr Asp Lys Leu Gly
405 410 415

Arg Cys Lys Arg Asp Ala Phe Val Ala Gly Leu Ser Phe Ala Gln Ala
420 425 430

Gly Gly Asn Trp Ala Asp Cys Phe
435 440

<210> 2
<211> 440
<212> PRT
<213> Aspergillus terreus cbs

<400> 2

Asn His Ser Asp Cys Thr Ser Val Asp Arg Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
20 25 30

Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr
35 40 45

Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser
50 55 60

Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser
85 90 95

Met Gly Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp
100 105 110

Leu Gly Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile
115 120 125

Asn Pro Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala
 130 135 140

Glu Lys Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His
 145 150 155 160

Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu
 165 170 175

Gly Thr Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe
 180 185 190

Glu Ala Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val
 195 200 205

Phe Ala Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val
 210 215 220

Gln Leu Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
 225 230 235 240

Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
 245 250 255

Asp Leu Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
 260 265 270

Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val
 275 280 285

Gln Gly Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
 290 295 300

Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro
 305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335

Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350

Lys Pro Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly

355

360

365

Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu
 370 375 380

Met Met Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly
 405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala
 420 425 430

Gly Gly Asn Trp Ala Glu Cys Phe
 435 440

<210> 3
 <211> 441
 <212> PRT
 <213> *Aspergillus niger* var. *awamori*

<400> 3

Asn Gln Ser Thr Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser
 1 5 10 15

Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
 20 25 30

Asn Glu Ser Ala Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
 35 40 45

Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
 50 55 60

Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
 65 70 75 80

Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
 115 120 125

Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
 130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
 145 150 155 160

Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
 165 170 175

Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
 180 185 190

Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
 195 200 205

Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
 210 215 220

Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
 225 230 235 240

Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
 245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Gln Ser
 260 265 270

Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
 275 280 285

Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 290 295 300

Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320

Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335

Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350

Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
 355 360 365

Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
 370 375 380

Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
 405 410 415

Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asp Trp Ala Glu Cys Ser Ala
 435 440

<210> 4
 <211> 441
 <212> PRT
 <213> Aspergillus niger T213

<400> 4

Asn Gln Ser Ser Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser
 1 5 10 15

Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
 20 25 30

Asn Glu Ser Val Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
 35 40 45

Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
 50 55 60

Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
 65 70 75 80

Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
 115 120 125

Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
 130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
 145 150 155 160

Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
 165 170 175

Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
 180 185 190

Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
 195 200 205

Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
 210 215 220

Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
 225 230 235 240

Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
 245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Arg Ser
 260 265 270

Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
 275 280 285

Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 290 295 300

Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320

Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335

Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350

Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
 355 360 365

Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
 370 375 380

Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
 405 410 415

Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asp Trp Ala Glu Cys Phe Ala
 435 440

<210> 5
 <211> 441
 <212> PRT
 <213> Aspergillus niger NRRL3135

<400> 5

Asn Gln Ser Ser Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser
 1 5 10 15

Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
 20 25 30

Asn Glu Ser Val Ile Ser Pro Glu Val Pro Ala Gly Cys Arg Val Thr
 35 40 45

Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser
 50 55 60

Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Ala

65		70		75		80
Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser	85		90		95	
Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn	100		105		110	
Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile	115		120		125	
Val Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly	130		135		140	
Lys Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg	145		150		155	160
Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu		165		170		175
Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe		180		185		190
Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr		195		200		205
Phe Val Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val		210		215		220
Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe		225		230		235
						240
Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys		245		250		255
Asp Leu Phe Thr His Asp Glu Trp Ile Asn Tyr Asp Tyr Leu Gln Ser		260		265		270
Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr		275		280		285
Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser		290		295		300

Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Ser Pro
305 310 315 320

Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
325 330 335

Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
340 345 350

Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
355 360 365

Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
370 375 380

Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Val Asp Ala Leu Gly
405 410 415

Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
420 425 430

Gly Gly Asp Trp Ala Glu Cys Phe Ala
435 440

<210> 6
<211> 440
<212> PRT
<213> *Aspergillus fumigatus* 13073

<400> 6

Gly Ser Lys Ser Cys Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro
1 5 10 15

Ala Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
20 25 30

Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln

275

280

285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
 290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
 305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
 325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
 340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
 355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
 385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
 405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
 420 425 430

Gly Asn Trp Gly Glu Cys Phe Ser
 435 440

<210> 7
 <211> 440
 <212> PRT
 <213> *Aspergillus fumigatus* 32722

<400> 7

Gly Ser Lys Ser Cys Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro
 1 5 10 15

Ala Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
 20 25 30

Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
 35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
 65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
 115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
 145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
 165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
 180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
 195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
 210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
 245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
 260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
 290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
 305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
 325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Gly
 340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
 355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
 385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
 405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
 420 425 430

Gly Asn Trp Gly Glu Cys Phe Ser
 435 440

<210> 8
 <211> 440
 <212> PRT
 <213> Aspergillus fumigatus 58128

<400> 8

Gly Ser Lys Ser Cys Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro
 1 5 10 15

Ala Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
 20 25 30

Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
 35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
 65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
 115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
 145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
 165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
 180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
 195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr
 210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Ser Leu Val Arg Ala Leu Ile Asn
385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
420 425 430

Gly Asn Trp Gly Glu Cys Phe Ser
435 440

<210> 9

<211> 440

<212> PRT

<213> Aspergillus fumigatus 26906

<400> 9

Gly Ser Lys Ser Cys Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro
1 5 10 15

Ala Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
20 25 30

Asp Glu Leu Ser Val Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr
35 40 45

Leu Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala
65 70 75 80

Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Ala Phe Gly Glu Gln Gln Leu Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser
165 170 175

Glu Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu
180 185 190

Ala Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe
195 200 205

Ala Pro Asp Ile Arg Ala Arg Ala Lys Lys His Leu Pro Gly Val Thr
210 215 220

Leu Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp
 225 230 235 240

Thr Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln
 245 250 255

Leu Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu
 260 265 270

Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln
 275 280 285

Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro
 290 295 300

Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala
 305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn
 325 330 335

Ser Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu
 340 345 350

Pro Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr
 355 360 365

Ser Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr
 370 375 380

Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn
 385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg
 405 410 415

Cys Lys Leu Asn Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly
 420 425 430

Gly Asn Trp Gly Glu Cys Phe Ser
 435 440

<210> 10
 <211> 440
 <212> PRT
 <213> Aspergillus fumigatus 32239

<400> 10

Gly Ser Lys Ala Cys Asp Thr Val Glu Leu Gly Tyr Gln Cys Ser Pro
 1 5 10 15

Gly Thr Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu
 20 25 30

Asp Glu Leu Ser Val Ser Ser Asp Leu Pro Lys Asp Cys Arg Val Thr
 35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ala Ser
 50 55 60

Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Lys Asn Ala
 65 70 75 80

Thr Glu Phe Lys Gly Lys Phe Ala Phe Leu Glu Thr Tyr Asn Tyr Thr
 85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn
 100 105 110

Ser Gly Ile Lys Phe Tyr Gln Lys Tyr Lys Ala Leu Ala Gly Ser Val
 115 120 125

Val Pro Phe Ile Arg Ser Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala Asn Val Ala Asp Pro Gly
 145 150 155 160

Ala Thr Asn Arg Ala Ala Pro Val Ile Ser Val Ile Ile Pro Glu Ser
 165 170 175

Glu Thr Tyr Asn Asn Thr Leu Asp His Ser Val Cys Thr Asn Phe Glu
 180 185 190

Ala Ser Glu Leu Gly Asp Glu Val Glu Ala Asn Phe Thr Ala Leu Phe

195	200	205
Ala Pro Ala Ile Arg Ala Arg Ile Glu Lys His Leu Pro Gly Val Gln 210	215	220
Leu Thr Asp Asp Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp 225	230	235 240
Thr Val Ala Arg Thr Ala Asp Ala Ser Glu Leu Ser Pro Phe Cys Ala 245	250	255
Ile Phe Thr His Asn Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu 260	265	270
Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln 275	280	285
Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Pro 290	295	300
Val Gln Asp His Thr Ser Thr Asn Ser Thr Leu Asp Ser Asp Pro Ala 305	310	315 320
Thr Phe Pro Leu Asn Ala Thr Ile Tyr Val Asp Phe Ser His Asp Asn 325	330	335
Gly Met Ile Pro Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Glu 340	345	350
Pro Leu Ser Gln Thr Ser Glu Glu Ser Thr Lys Glu Ser Asn Gly Tyr 355	360	365
Ser Ala Ser Trp Ala Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr 370	375	380
Met Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn 385	390	395 400
Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg 405	410	415
Cys Lys Leu Lys Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly 420	425	430

Gly Asn Ser Glu Gln Ser Phe Ser
435 440

<210> 11
<211> 439
<212> PRT
<213> Emericella nidulans

<400> 11

Gln Asn His Ser Cys Asn Thr Ala Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Asn Val Ser His Val Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Ile Glu
20 25 30

Gln Glu Ser Ala Ile Ser Glu Asp Val Pro His Gly Cys Glu Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
50 55 60

Lys Ser Lys Ala Tyr Ser Gly Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ser Phe Trp Gly Gln Tyr Ala Phe Leu Glu Ser Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Ile Phe Gly Glu Asn Gln Met Val Asp
100 105 110

Ser Gly Ala Lys Phe Tyr Arg Arg Tyr Lys Asn Leu Ala Arg Lys Asn
115 120 125

Thr Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Val Ala Ser Ala
130 135 140

Glu Lys Phe Ile Asn Gly Phe Arg Lys Ala Gln Leu His Asp His Gly
145 150 155 160

Ser Gly Gln Ala Thr Pro Val Val Asn Val Ile Ile Pro Glu Ile Asp
165 170 175

Gly Phe Asn Asn Thr Leu Asp His Ser Thr Cys Val Ser Phe Glu Asn
180 185 190

Asp Glu Arg Ala Asp Glu Ile Glu Ala Asn Phe Thr Ala Ile Met Gly
195 200 205

Pro Pro Ile Arg Lys Arg Leu Glu Asn Asp Leu Pro Gly Ile Lys Leu
210 215 220

Thr Asn Glu Asn Val Ile Tyr Leu Met Asp Met Cys Ser Phe Asp Thr
225 230 235 240

Met Ala Arg Thr Ala His Gly Thr Glu Leu Ser Pro Phe Cys Ala Ile
245 250 255

Phe Thr Glu Lys Glu Trp Leu Gln Tyr Asp Tyr Leu Gln Ser Leu Ser
260 265 270

Lys Tyr Tyr Gly Tyr Gly Ala Gly Ser Pro Leu Gly Pro Ala Gln Gly
275 280 285

Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Gln Ser Pro Val
290 295 300

Gln Asp Asn Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr
305 310 315 320

Phe Pro Leu Asp Arg Lys Leu Tyr Ala Asp Phe Ser His Asp Asn Ser
325 330 335

Met Ile Ser Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Gln Pro
340 345 350

Leu Ser Met Asp Ser Val Glu Ser Ile Gln Glu Met Asp Gly Tyr Ala
355 360 365

Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Leu Met
370 375 380

Gln Cys Glu Lys Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg
385 390 395 400

Val Val Pro Leu His Gly Cys Ala Val Asp Lys Phe Gly Arg Cys Thr

405

410

415

Leu Asp Asp Trp Val Glu Gly Leu Asn Phe Ala Arg Ser Gly Gly Asn
 420 425 430

Trp Lys Thr Cys Phe Thr Leu
 435

<210> 12

<211> 443

<212> PRT

<213> Talaromyces Thermophilus

<400> 12

Asp Ser His Ser Cys Asn Thr Val Glu Gly Gly Tyr Gln Cys Arg Pro
 1 5 10 15

Glu Ile Ser His Ser Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala
 20 25 30

Asp Gln Ser Glu Ile Ser Pro Asp Val Pro Gln Asn Cys Lys Ile Thr
 35 40 45

Phe Val Gln Leu Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
 50 55 60

Lys Thr Glu Leu Tyr Ser Gln Leu Ile Ser Arg Ile Gln Lys Thr Ala
 65 70 75 80

Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe Leu Lys Asp Tyr Arg Tyr Gln
 85 90 95

Leu Gly Ala Asn Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Ile Gln
 100 105 110

Leu Gly Ile Lys Phe Tyr Asn His Tyr Lys Ser Leu Ala Arg Asn Ala
 115 120 125

Val Pro Phe Val Arg Cys Ser Gly Ser Asp Arg Val Ile Ala Ser Gly
 130 135 140

Arg Leu Phe Ile Glu Gly Phe Gln Ser Ala Lys Val Leu Asp Pro His
 145 150 155 160

Ser Asp Lys His Asp Ala Pro Pro Thr Ile Asn Val Ile Ile Glu Glu
165 170 175

Gly Pro Ser Tyr Asn Asn Thr Leu Asp Thr Gly Ser Cys Pro Val Phe
180 185 190

Glu Asp Ser Ser Gly Gly His Asp Ala Gln Glu Lys Phe Ala Lys Gln
195 200 205

Phe Ala Pro Ala Ile Leu Glu Lys Ile Lys Asp His Leu Pro Gly Val
210 215 220

Asp Leu Ala Val Ser Asp Val Pro Tyr Leu Met Asp Leu Cys Pro Phe
225 230 235 240

Glu Thr Leu Ala Arg Asn His Thr Asp Thr Leu Ser Pro Phe Cys Ala
245 250 255

Leu Ser Thr Gln Glu Glu Trp Gln Ala Tyr Asp Tyr Tyr Gln Ser Leu
260 265 270

Gly Lys Tyr Tyr Gly Asn Gly Gly Gly Asn Pro Leu Gly Pro Ala Gln
275 280 285

Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met Thr His Ser Pro
290 295 300

Val Gln Asp Tyr Thr Thr Val Asn His Thr Leu Asp Ser Asn Pro Ala
305 310 315 320

Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn
325 330 335

Thr Met Thr Ser Ile Phe Ala Ala Leu Gly Leu Tyr Asn Gly Thr Ala
340 345 350

Lys Leu Ser Thr Thr Glu Ile Lys Ser Ile Glu Glu Thr Asp Gly Tyr
355 360 365

Ser Ala Ala Trp Thr Val Pro Phe Gly Gly Arg Ala Tyr Ile Glu Met
370 375 380

Met Gln Cys Asp Asp Ser Asp Glu Pro Val Val Arg Val Leu Val Asn
 385 390 395 400

Asp Arg Val Val Pro Leu His Gly Cys Glu Val Asp Ser Leu Gly Arg
 405 410 415

Cys Lys Arg Asp Asp Phe Val Arg Gly Leu Ser Phe Ala Arg Gln Gly
 420 425 430

Gly Asn Trp Glu Gly Cys Tyr Ala Ala Ser Glu
 435 440

<210> 13
 <211> 466
 <212> PRT
 <213> Myceliophthora thermophila

<400> 13

Glu Ser Arg Pro Cys Asp Thr Pro Asp Leu Gly Phe Gln Cys Gly Thr
 1 5 10 15

Ala Ile Ser His Phe Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Val Pro
 20 25 30

Ser Glu Leu Asp Ala Ser Ile Pro Asp Asp Cys Glu Val Thr Phe Ala
 35 40 45

Gln Val Leu Ser Arg His Gly Ala Arg Ala Pro Thr Leu Lys Arg Ala
 50 55 60

Ala Ser Tyr Val Asp Leu Ile Asp Arg Ile His His Gly Ala Ile Ser
 65 70 75 80

Tyr Gly Pro Gly Tyr Glu Phe Leu Arg Thr Tyr Asp Tyr Thr Leu Gly
 85 90 95

Ala Asp Glu Leu Thr Arg Thr Gly Gln Gln Gln Met Val Asn Ser Gly
 100 105 110

Ile Lys Phe Tyr Arg Arg Tyr Arg Ala Leu Ala Arg Lys Ser Ile Pro
 115 120 125

Phe Val Arg Thr Ala Gly Gln Asp Arg Val Val His Ser Ala Glu Asn
 130 135 140

Phe Thr Gln Gly Phe His Ser Ala Leu Leu Ala Asp Arg Gly Ser Thr
 145 150 155 160

Val Arg Pro Thr Leu Pro Tyr Asp Met Val Val Ile Pro Glu Thr Ala
 165 170 175

Gly Ala Asn Asn Thr Leu His Asn Asp Leu Cys Thr Ala Phe Glu Glu
 180 185 190

Gly Pro Tyr Ser Thr Ile Gly Asp Asp Ala Gln Asp Thr Tyr Leu Ser
 195 200 205

Thr Phe Ala Gly Pro Ile Thr Ala Arg Val Asn Ala Asn Leu Pro Gly
 210 215 220

Ala Asn Leu Thr Asp Ala Asp Thr Val Ala Leu Met Asp Leu Cys Pro
 225 230 235 240

Phe Glu Thr Val Ala Ser Ser Ser Ser Asp Pro Ala Thr Ala Asp Ala
 245 250 255

Gly Gly Gly Asn Gly Arg Pro Leu Ser Pro Phe Cys Arg Leu Phe Ser
 260 265 270

Glu Ser Glu Trp Arg Ala Tyr Asp Tyr Leu Gln Ser Val Gly Lys Trp
 275 280 285

Tyr Gly Tyr Gly Pro Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly
 290 295 300

Phe Val Asn Glu Leu Leu Ala Arg Leu Ala Gly Val Pro Val Arg Asp
 305 310 315 320

Gly Thr Ser Thr Asn Arg Thr Leu Asp Gly Asp Pro Arg Thr Phe Pro
 325 330 335

Leu Gly Arg Pro Leu Tyr Ala Asp Phe Ser His Asp Asn Asp Met Met
 340 345 350

Gly Val Leu Gly Ala Leu Gly Ala Tyr Asp Gly Val Pro Pro Leu Asp
 355 360 365

Lys Thr Ala Arg Arg Asp Pro Glu Glu Leu Gly Gly Tyr Ala Ala Ser
370 375 380

Trp Ala Val Pro Phe Ala Ala Arg Ile Tyr Val Glu Lys Met Arg Cys
385 390 395 400

Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Gly Arg Gln Glu Lys
405 410 415

Asp Glu Glu Met Val Arg Val Leu Val Asn Asp Arg Val Met Thr Leu
420 425 430

Lys Gly Cys Gly Ala Asp Glu Arg Gly Met Cys Thr Leu Glu Arg Phe
435 440 445

Ile Glu Ser Met Ala Phe Ala Arg Gly Asn Gly Lys Trp Asp Leu Cys
450 455 460

Phe Ala
465

<210> 14
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 14

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu
20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ser Gln Pro His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu
165 170 175

Gly Ser Gly Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe
180 185 190

Glu Asp Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu
195 200 205

Phe Ala Pro Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val
210 215 220

Thr Leu Thr Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe
225 230 235 240

Glu Thr Val Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys
245 250 255

Ala Leu Phe Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
275 280 285

Gln Gly Val Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
290 295 300

Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335

Asn Ser Met Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350

Ala Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
 355 360 365

Tyr Ser Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu
 370 375 380

Met Met Gln Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly
 405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asn Trp Ala Glu Cys Phe Ala
 435 440

<210> 15
 <211> 1426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (12)..(1412)
 <223>

<220>
 <221> sig_peptide
 <222> (12)..(89)
 <223>

<220>
 <221> mat_peptide

<222> (90) .. ()

<223>

<400> 15

tatatgaatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg	50
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu	
-25 -20 -15	
ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac	98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His	
-10 -5 -1 1	
tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct	146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser	
5 10 15	
cac ttg tgg ggt caa tac tct cca tac ttc tct ttg gaa gac gaa tct	194
His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser	
20 25 30 35	
gct att tct cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa	242
Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln	
40 45 50	
gtt ttg tct aga cac ggt gct aga tac cca act tct tct aag tct aag	290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys	
55 60 65	
gct tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc	338
Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe	
70 75 80	
aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct	386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala	
85 90 95	
gac gac ttg act cca ttc ggt gaa aac caa atg gtt aac tct ggt att	434
Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile	
100 105 110 115	
aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc	482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe	
120 125 130	
att aga gct tct ggt tct gac aga gtt att gct tct gct gaa aag ttc	530
Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe	
135 140 145	
att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt tct caa cca	578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro	
150 155 160	
cac caa gct tct cca gtt att gac gtt att att cca gaa gga tcc ggt	626
His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu Gly Ser Gly	
165 170 175	
tac aac aac act ttg gac cac ggt act tgt act gct ttc gaa gac tct	674

Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser	
180 185 190 195	
gaa ttg ggt gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca	722
Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro	
200 205 210	
gct att aga gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act	770
Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr	
215 220 225	
gac gaa gac gtt gtt tac ttg atg gac atg tgt cca ttc gaa act gtt	818
Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe Glu Thr Val	
230 235 240	
gct aga act tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc	866
Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe	
245 250 255	
act cac gac gaa tgg aga caa tac gac tac ttg caa tct ttg ggt aag	914
Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys	
260 265 270 275	
tac tac ggt tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt	962
Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val	
280 285 290	
ggt ttc gct aac gaa ttg att gct aga ttg act aga tct cca gtt caa	1010
Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln	
295 300 305	
gac cac act tct act aac cac act ttg gac tct aac cca gct act ttc	1058
Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe	
310 315 320	
cca ttg aac gct act ttg tac gct gac ttc tct cac gac aac tct atg	1106
Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Ser Met	
325 330 335	
att tct att ttc ttc gct ttg ggt ttg tac aac ggt act gct cca ttg	1154
Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu	
340 345 350 355	
tct act act tct gtt gaa tct att gaa gaa act gac ggt tac tct gct	1202
Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala	
360 365 370	
tct tgg act gtt cca ttc ggt gct aga gct tac gtt gaa atg atg caa	1250
Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu Met Met Gln	
375 380 385	
tgt caa gct gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga	1298
Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg	
390 395 400	
ggt gtt cca ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag	1346
Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys	

405	410	415	
aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac			1394
Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn			
420	425	430	435
tgg gct gaa tgt ttc gct taagaattca tata			1426
Trp Ala Glu Cys Phe Ala			
440			
<210> 16			
<211> 467			
<212> PRT			
<213> Artificial Sequence			
<220>			
<223> Synthetic			
<400> 16			
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser			
-25	-20	-15	
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp			
-10	-5	-1 1	5
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp			
10	15		20
Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser Ala Ile Ser			
25	30		35
Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser			
40	45		50
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser			
55	60	65	70
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys			
75	80		85
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu			
90	95		100
Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr			
105	110		115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
 155 160 165

Ser Pro Val Ile Asp Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
 170 175 180

Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly
 185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
 200 205 210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
 215 220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Glu Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260

Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
 280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
 295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Ser Met Ile Ser Ile
 330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu Ser Thr Thr

345

350

355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 360 365 370

Val Pro Phe Gly Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435

Cys Phe Ala
 440

<210> 17
 <211> 422
 <212> PRT
 <213> Paxillus involutus phyA1

<400> 17

Ser Val Pro Lys Asn Thr Ala Pro Thr Phe Pro Ile Pro Glu Ser Glu
 1 5 10 15

Gln Arg Asn Trp Ser Pro Tyr Ser Pro Tyr Phe Pro Leu Ala Glu Tyr
 20 25 30

Lys Ala Pro Pro Ala Gly Cys Gln Ile Asn Gln Val Asn Ile Ile Gln
 35 40 45

Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Thr Thr Arg Ile Lys
 50 55 60

Ala Gly Leu Thr Lys Leu Gln Gly Val Gln Asn Phe Thr Asp Ala Lys
 65 70 75 80

Phe Asn Phe Ile Lys Ser Phe Lys Tyr Asp Leu Gly Asn Ser Asp Leu
 85 90 95

Val Pro Phe Gly Ala Ala Gln Ser Phe Asp Ala Gly Gln Glu Ala Phe
 100 105 110

Ala Arg Tyr Ser Lys Leu Val Ser Lys Asn Asn Leu Pro Phe Ile Arg
 115 120 125

Ala Asp Gly Ser Asp Arg Val Val Asp Ser Ala Thr Asn Trp Thr Ala
 130 135 140

Gly Phe Ala Ser Ala Ser His Asn Thr Val Gln Pro Lys Leu Asn Leu
 145 150 155 160

Ile Leu Pro Gln Thr Gly Asn Asp Thr Leu Glu Asp Asn Met Cys Pro
 165 170 175

Ala Ala Gly Asp Ser Asp Pro Gln Val Asn Ala Trp Leu Ala Val Ala
 180 185 190

Phe Pro Ser Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro Ser Val Asn
 195 200 205

Leu Thr Asp Thr Asp Ala Phe Asn Leu Val Ser Leu Cys Ala Phe Leu
 210 215 220

Thr Val Ser Lys Glu Lys Lys Ser Asp Phe Cys Thr Leu Phe Glu Gly
 225 230 235 240

Ile Pro Gly Ser Phe Glu Ala Phe Ala Tyr Gly Gly Asp Leu Asp Lys
 245 250 255

Phe Tyr Gly Thr Gly Tyr Gly Gln Glu Leu Gly Pro Val Gln Gly Val
 260 265 270

Gly Tyr Val Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Ala Val Arg
 275 280 285

Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ala Ser Pro Val Thr Phe
 290 295 300

Pro Leu Asn Lys Thr Phe Tyr Ala Asp Phe Ser His Asp Asn Leu Met
 305 310 315 320

Val Ala Val Phe Ser Ala Met Gly Leu Phe Arg Gln Pro Ala Pro Leu
325 330 335

Ser Thr Ser Val Pro Asn Pro Trp Arg Thr Trp Arg Thr Ser Ser Leu
340 345 350

Val Pro Phe Ser Gly Arg Met Val Val Glu Arg Leu Ser Cys Phe Gly
355 360 365

Thr Thr Lys Val Arg Val Leu Val Gln Asp Gln Val Gln Pro Leu Glu
370 375 380

Phe Cys Gly Gly Asp Arg Asn Gly Leu Cys Thr Leu Ala Lys Phe Val
385 390 395 400

Glu Ser Gln Thr Phe Ala Arg Ser Asp Gly Ala Gly Asp Phe Glu Lys
405 410 415

Cys Phe Ala Thr Ser Ala
420

<210> 18
<211> 422
<212> PRT
<213> Paxillus involutus phyA2

<400> 18

Ser Val Pro Arg Asn Ile Ala Pro Lys Phe Ser Ile Pro Glu Ser Glu
1 5 10 15

Gln Arg Asn Trp Ser Pro Tyr Ser Pro Tyr Phe Pro Leu Ala Glu Tyr
20 25 30

Lys Ala Pro Pro Ala Gly Cys Glu Ile Asn Gln Val Asn Ile Ile Gln
35 40 45

Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Thr Arg Ile Lys
50 55 60

Ala Gly Leu Ser Lys Leu Gln Ser Val Gln Asn Phe Thr Asp Pro Lys
65 70 75 80

Phe Asp Phe Ile Lys Ser Phe Thr Tyr Asp Leu Gly Thr Ser Asp Leu
85 90 95

Val Pro Phe Gly Ala Ala Gln Ser Phe Asp Ala Gly Leu Glu Val Phe
100 105 110

Ala Arg Tyr Ser Lys Leu Val Ser Ser Asp Asn Leu Pro Phe Ile Arg
115 120 125

Ser Asp Gly Ser Asp Arg Val Val Asp Thr Ala Thr Asn Trp Thr Ala
130 135 140

Gly Phe Ala Ser Ala Ser Arg Asn Ala Ile Gln Pro Lys Leu Asp Leu
145 150 155 160

Ile Leu Pro Gln Thr Gly Asn Asp Thr Leu Glu Asp Asn Met Cys Pro
165 170 175

Ala Ala Gly Glu Ser Asp Pro Gln Val Asp Ala Trp Leu Ala Ser Ala
180 185 190

Phe Pro Ser Val Thr Ala Gln Leu Asn Ala Ala Ala Pro Gly Ala Asn
195 200 205

Leu Thr Asp Ala Asp Ala Phe Asn Leu Val Ser Leu Cys Pro Phe Met
210 215 220

Thr Val Ser Lys Glu Gln Lys Ser Asp Phe Cys Thr Leu Phe Glu Gly
225 230 235 240

Ile Pro Gly Ser Phe Glu Ala Phe Ala Tyr Ala Gly Asp Leu Asp Lys
245 250 255

Phe Tyr Gly Thr Gly Tyr Gly Gln Ala Leu Gly Pro Val Gln Gly Val
260 265 270

Gly Tyr Ile Asn Glu Leu Leu Ala Arg Leu Thr Asn Ser Ala Val Asn
275 280 285

Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ala Ala Pro Asp Thr Phe
290 295 300

Pro Leu Asn Lys Thr Met Tyr Ala Asp Phe Ser His Asp Asn Leu Met
305 310 315 320

Val Ala Val Phe Ser Ala Met Gly Leu Phe Arg Gln Ser Ala Pro Leu
325 330 335

Ser Thr Ser Thr Pro Asp Pro Asn Arg Thr Trp Leu Thr Ser Ser Val
340 345 350

Val Pro Phe Ser Ala Arg Met Ala Val Glu Arg Leu Ser Cys Ala Gly
355 360 365

Thr Thr Lys Val Arg Val Leu Val Gln Asp Gln Val Gln Pro Leu Glu
370 375 380

Phe Cys Gly Gly Asp Gln Asp Gly Leu Cys Ala Leu Asp Lys Phe Val
385 390 395 400

Glu Ser Gln Ala Tyr Ala Arg Ser Gly Gly Ala Gly Asp Phe Glu Lys
405 410 415

Cys Leu Ala Thr Thr Val
420

<210> 19
<211> 420
<212> PRT
<213> Trametes Pubescens

<400> 19

His Ile Pro Leu Arg Asp Thr Ser Ala Cys Leu Asp Val Thr Arg Asp
1 5 10 15

Val Gln Gln Ser Trp Ser Met Tyr Ser Pro Tyr Phe Pro Ala Ala Thr
20 25 30

Tyr Val Ala Pro Pro Ala Ser Cys Gln Ile Asn Gln Val His Ile Ile
35 40 45

Gln Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Lys Arg Ile
50 55 60

Gln Thr Ala Val Ala Lys Leu Lys Ala Ala Ser Asn Tyr Thr Asp Pro
65 70 75 80

Leu Leu Ala Phe Val Thr Asn Tyr Thr Tyr Ser Leu Gly Gln Asp Ser

85

90

95

Leu Val Glu Leu Gly Ala Thr Gln Ser Ser Glu Ala Gly Gln Glu Ala
 100 105 110

Phe Thr Arg Tyr Ser Ser Leu Val Ser Ala Asp Glu Leu Pro Phe Val
 115 120 125

Arg Ala Ser Gly Ser Asp Arg Val Val Ala Thr Ala Asn Asn Trp Thr
 130 135 140

Ala Gly Phe Ala Leu Ala Ser Ser Asn Ser Ile Thr Pro Val Leu Ser
 145 150 155 160

Val Ile Ile Ser Glu Ala Gly Asn Asp Thr Leu Asp Asp Asn Met Cys
 165 170 175

Pro Ala Ala Gly Asp Ser Asp Pro Gln Val Asn Gln Trp Leu Ala Gln
 180 185 190

Phe Ala Pro Pro Met Thr Ala Arg Leu Asn Ala Gly Ala Pro Gly Ala
 195 200 205

Asn Leu Thr Asp Thr Asp Thr Tyr Asn Leu Leu Thr Leu Cys Pro Phe
 210 215 220

Glu Thr Val Ala Thr Glu Arg Arg Ser Glu Phe Cys Asp Ile Tyr Glu
 225 230 235 240

Glu Leu Gln Ala Glu Asp Ala Phe Ala Tyr Asn Ala Asp Leu Asp Lys
 245 250 255

Phe Tyr Gly Thr Gly Tyr Gly Gln Pro Leu Gly Pro Val Gln Gly Val
 260 265 270

Gly Tyr Ile Asn Glu Leu Ile Ala Arg Leu Thr Ala Gln Asn Val Ser
 275 280 285

Asp His Thr Gln Thr Asn Ser Thr Leu Asp Ser Ser Pro Glu Thr Phe
 290 295 300

Pro Leu Asn Arg Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gln Met
 305 310 315 320

Val Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln Ser Ala Pro Leu
 325 330 335

Asp Pro Thr Thr Pro Asp Pro Ala Arg Thr Phe Leu Val Lys Lys Ile
 340 345 350

Val Pro Phe Ser Ala Arg Met Val Val Glu Arg Leu Asp Cys Gly Gly
 355 360 365

Ala Gln Ser Val Arg Leu Leu Val Asn Asp Ala Val Gln Pro Leu Ala
 370 375 380

Phe Cys Gly Ala Asp Thr Ser Gly Val Cys Thr Leu Asp Ala Phe Val
 385 390 395 400

Glu Ser Gln Ala Tyr Ala Arg Asn Asp Gly Glu Gly Asp Phe Glu Lys
 405 410 415

Cys Phe Ala Thr
 420

<210> 20
 <211> 435
 <212> PRT
 <213> Agrocybe peidades

<400> 20

Gly Gly Val Val Gln Ala Thr Phe Val Gln Pro Phe Phe Pro Pro Gln
 1 5 10 15

Ile Gln Asp Ser Trp Ala Ala Tyr Thr Pro Tyr Tyr Pro Val Gln Ala
 20 25 30

Tyr Thr Pro Pro Pro Lys Asp Cys Lys Ile Thr Gln Val Asn Ile Ile
 35 40 45

Gln Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Gly Thr Arg Ile
 50 55 60

Gln Ala Ala Val Lys Lys Leu Gln Ser Ala Lys Thr Tyr Thr Asp Pro
 65 70 75 80

Arg Leu Asp Phe Leu Thr Asn Tyr Thr Tyr Thr Leu Gly His Asp Asp
85 90 95

Leu Val Pro Phe Gly Ala Leu Gln Ser Ser Gln Ala Gly Glu Glu Thr
100 105 110

Phe Gln Arg Tyr Ser Phe Leu Val Ser Lys Glu Asn Leu Pro Phe Val
115 120 125

Arg Ala Ser Ser Ser Asn Arg Val Val Asp Ser Ala Thr Asn Trp Thr
130 135 140

Glu Gly Phe Ser Ala Ala Ser His His Val Leu Asn Pro Ile Leu Phe
145 150 155 160

Val Ile Leu Ser Glu Ser Leu Asn Asp Thr Leu Asp Asp Ala Met Cys
165 170 175

Pro Asn Ala Gly Ser Ser Asp Pro Gln Thr Gly Ile Trp Thr Ser Ile
180 185 190

Tyr Gly Thr Pro Ile Ala Asn Arg Leu Asn Gln Gln Ala Pro Gly Ala
195 200 205

Asn Ile Thr Ala Ala Asp Val Ser Asn Leu Ile Pro Leu Cys Ala Phe
210 215 220

Glu Thr Ile Val Lys Glu Thr Pro Ser Pro Phe Cys Asn Leu Phe Thr
225 230 235 240

Pro Glu Glu Phe Ala Gln Phe Glu Tyr Phe Gly Asp Leu Asp Lys Phe
245 250 255

Tyr Gly Thr Gly Tyr Gly Gln Pro Leu Gly Pro Val Gln Gly Val Gly
260 265 270

Tyr Ile Asn Glu Leu Leu Ala Arg Leu Thr Glu Met Pro Val Arg Asp
275 280 285

Asn Thr Gln Thr Asn Arg Thr Leu Asp Ser Ser Pro Leu Thr Phe Pro
290 295 300

Leu Asp Arg Ser Ile Tyr Ala Asp Leu Ser His Asp Asn Gln Met Ile

Val Ala Ala Val Ala Lys Ile Gln Met Ala Arg Pro Phe Thr Asp Pro
65 70 75 80

Lys Tyr Glu Phe Leu Asn Asp Phe Val Tyr Lys Phe Gly Val Ala Asp
85 90 95

Leu Leu Pro Phe Gly Ala Asn Gln Ser His Gln Thr Gly Thr Asp Met
100 105 110

Tyr Thr Arg Tyr Ser Thr Leu Phe Glu Gly Gly Asp Val Pro Phe Val
115 120 125

Arg Ala Ala Gly Asp Gln Arg Val Val Asp Ser Ser Thr Asn Trp Thr
130 135 140

Ala Gly Phe Gly Asp Ala Ser Gly Glu Thr Val Leu Pro Thr Leu Gln
145 150 155 160

Val Val Leu Gln Glu Glu Gly Asn Cys Thr Leu Cys Asn Asn Met Cys
165 170 175

Pro Asn Glu Val Asp Gly Asp Glu Ser Thr Thr Trp Leu Gly Val Phe
180 185 190

Ala Pro Asn Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro Ser Ala Asn
195 200 205

Leu Ser Asp Ser Asp Ala Leu Thr Leu Met Asp Met Cys Pro Phe Asp
210 215 220

Thr Leu Ser Ser Gly Asn Ala Ser Pro Phe Cys Asp Leu Phe Thr Ala
225 230 235 240

Glu Glu Tyr Val Ser Tyr Glu Tyr Tyr Tyr Asp Leu Asp Lys Tyr Tyr
245 250 255

Gly Thr Gly Pro Gly Asn Ala Leu Gly Pro Val Gln Gly Val Gly Tyr
260 265 270

Val Asn Glu Leu Leu Ala Arg Leu Thr Gly Gln Ala Val Arg Asp Glu
275 280 285

Thr Gln Thr Asn Arg Thr Leu Asp Ser Asp Pro Ala Thr Phe Pro Leu
 290 295 300

Asn Arg Thr Phe Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Pro
 305 310 315 320

Ile Phe Ala Ala Leu Gly Leu Phe Asn Ala Thr Ala Leu Asp Pro Leu
 325 330 335

Lys Pro Asp Glu Asn Arg Leu Trp Val Asp Ser Lys Leu Val Pro Phe
 340 345 350

Ser Gly His Met Thr Val Glu Lys Leu Ala Cys Ser Gly Lys Glu Ala
 355 360 365

Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu Glu Phe Cys Gly
 370 375 380

Gly Val Asp Gly Val Cys Glu Leu Ser Ala Phe Val Glu Ser Gln Thr
 385 390 395 400

Tyr Ala Arg Glu Asn Gly Gln Gly Asp Phe Ala Lys Cys Gly Phe Val
 405 410 415

Pro Ser Glu

<210> 22
 <211> 369
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 22

Ser Pro Arg Thr Ala Ala Gln Leu Pro Ile Pro Gln Gln Trp Ser Pro
 1 5 10 15

Tyr Ser Pro Tyr Phe Pro Val Ala Tyr Ala Pro Pro Ala Gly Cys Gln
 20 25 30

Ile Gln Val Asn Ile Ile Gln Arg His Gly Ala Arg Phe Pro Thr Ser
 35 40 45

Gly Ala Ala Thr Arg Ile Gln Ala Ala Val Ala Lys Leu Gln Ser Ala
50 55 60

Thr Asp Pro Lys Leu Asp Phe Leu Asn Thr Tyr Leu Gly Asp Asp Leu
65 70 75 80

Val Pro Phe Gly Ala Gln Ser Ser Gln Ala Gly Gln Glu Ala Phe Thr
85 90 95

Arg Tyr Ser Leu Val Ser Asp Asn Leu Pro Phe Val Arg Ala Ser Gly
100 105 110

Ser Asp Arg Val Val Asp Ser Ala Thr Asn Trp Thr Ala Gly Phe Ala
115 120 125

Ala Ser Asn Thr Pro Leu Val Ile Leu Ser Glu Gly Asn Asp Thr Leu
130 135 140

Asp Asp Asn Met Cys Pro Ala Gly Asp Ser Asp Pro Gln Asn Trp Leu
145 150 155 160

Ala Val Phe Ala Pro Pro Ile Thr Ala Arg Leu Asn Ala Ala Ala Pro
165 170 175

Gly Ala Asn Leu Thr Asp Asp Ala Asn Leu Leu Cys Pro Phe Glu Thr
180 185 190

Val Ser Glu Ser Phe Cys Asp Leu Phe Glu Pro Glu Glu Phe Ala Phe
195 200 205

Tyr Gly Asp Leu Asp Lys Phe Tyr Gly Thr Gly Tyr Gly Gln Pro Leu
210 215 220

Gly Pro Val Gln Gly Val Gly Tyr Ile Asn Glu Leu Leu Ala Arg Leu
225 230 235 240

Thr Gln Ala Val Arg Asp Asn Thr Gln Thr Asn Arg Thr Leu Asp Ser
245 250 255

Ser Pro Thr Phe Pro Leu Asn Arg Thr Phe Tyr Ala Asp Phe Ser His
260 265 270

Asp Asn Gln Met Val Ala Ile Phe Ser Ala Met Gly Leu Phe Asn Gln
 275 280 285

Ser Ala Pro Leu Asp Pro Ser Pro Asp Pro Asn Arg Thr Trp Val Thr
 290 295 300

Ser Lys Leu Val Pro Phe Ser Ala Arg Met Val Val Glu Arg Leu Cys
 305 310 315 320

Gly Thr Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu Glu Phe
 325 330 335

Cys Gly Gly Asp Asp Gly Cys Thr Leu Asp Ala Phe Val Glu Ser Gln
 340 345 350

Tyr Ala Arg Glu Asp Gly Gln Gly Asp Phe Glu Lys Cys Phe Ala Thr
 355 360 365

Pro

<210> 23
 <211> 440
 <212> PRT
 <213> Thermomyces lanuginosus

<400> 23

Asn Val Asp Ile Ala Arg His Trp Gly Gln Tyr Ser Pro Phe Phe Ser
 1 5 10 15

Leu Ala Glu Val Ser Glu Ile Ser Pro Ala Val Pro Lys Gly Cys Arg
 20 25 30

Val Glu Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr
 35 40 45

Ala His Lys Ser Glu Val Tyr Ala Glu Leu Leu Gln Arg Ile Gln Asp
 50 55 60

Thr Ala Thr Glu Phe Lys Gly Asp Phe Ala Phe Leu Arg Asp Tyr Ala
 65 70 75 80

Tyr His Leu Gly Ala Asp Asn Leu Thr Arg Phe Gly Glu Glu Gln Met
 85 90 95

Met Glu Ser Gly Arg Gln Phe Tyr His Arg Tyr Arg Glu Gln Ala Arg
100 105 110

Glu Ile Val Pro Phe Val Arg Ala Ala Gly Ser Ala Arg Val Ile Ala
115 120 125

Ser Ala Glu Phe Phe Asn Arg Gly Phe Gln Asp Ala Lys Asp Arg Asp
130 135 140

Pro Arg Ser Asn Lys Asp Gln Ala Glu Pro Val Ile Asn Val Ile Ile
145 150 155 160

Ser Glu Glu Thr Gly Ser Asn Asn Thr Leu Asp Gly Leu Thr Cys Pro
165 170 175

Ala Ala Glu Glu Ala Pro Asp Pro Thr Gln Pro Ala Glu Phe Leu Gln
180 185 190

Val Phe Gly Pro Arg Val Leu Lys Lys Ile Thr Lys His Met Pro Gly
195 200 205

Val Asn Leu Thr Leu Glu Asp Val Pro Leu Phe Met Asp Leu Cys Pro
210 215 220

Phe Asp Thr Val Gly Ser Asp Pro Val Leu Phe Pro Arg Gln Leu Ser
225 230 235 240

Pro Phe Cys His Leu Phe Thr Ala Asp Asp Trp Met Ala Tyr Asp Tyr
245 250 255

Tyr Tyr Thr Leu Asp Lys Tyr Tyr Ser His Gly Gly Gly Ser Ala Phe
260 265 270

Gly Pro Ser Arg Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met
275 280 285

Thr Gly Asn Leu Pro Val Lys Asp His Thr Thr Val Asn His Thr Leu
290 295 300

Asp Asp Asn Pro Glu Thr Phe Pro Leu Asp Ala Val Leu Tyr Ala Asp
305 310 315 320

Phe Ser His Asp Asn Thr Met Thr Gly Ile Phe Ser Ala Met Gly Leu
325 330 335

Tyr Asn Gly Thr Lys Pro Leu Ser Thr Ser Lys Ile Gln Pro Pro Thr
340 345 350

Gly Ala Ala Ala Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala
355 360 365

Ala Arg Ala Tyr Val Glu Leu Leu Arg Cys Glu Thr Glu Thr Ser Ser
370 375 380

Glu Glu Glu Glu Glu Gly Glu Asp Glu Pro Phe Val Arg Val Leu Val
385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Arg Val Asp Arg Trp Gly
405 410 415

Arg Cys Arg Arg Asp Glu Trp Ile Lys Gly Leu Thr Phe Ala Arg Gln
420 425 430

Gly Gly His Trp Asp Arg Cys Phe
435 440

<210> 24
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 24

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala
20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr
35 40 45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
115 120 125

Val Pro Phe Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ala Asn Pro His Gln Ala Ser Pro Val Ile Asn Val Ile Ile Pro Glu
165 170 175

Gly Ala Gly Tyr Asn Asn Thr Leu Asp His Gly Leu Cys Thr Ala Phe
180 185 190

Glu Glu Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Val
195 200 205

Phe Ala Pro Pro Ile Arg Ala Arg Leu Glu Ala His Leu Pro Gly Val
210 215 220

Asn Leu Thr Asp Glu Asp Val Val Asn Leu Met Asp Met Cys Pro Phe
225 230 235 240

Asp Thr Val Ala Arg Thr Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys
245 250 255

Asp Leu Phe Thr His Asp Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
275 280 285

Gln Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 290 295 300

Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335

Asn Thr Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350

Lys Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
 355 360 365

Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu
 370 375 380

Met Met Gln Cys Glu Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly
 405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asn Trp Glu Glu Cys Phe Ala
 435 440

<210> 25
 <211> 1426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (12) .. (1412)
 <223>

<220>
 <221> mat_peptide
 <222> (90) .. ()

<223>

<220>

<221> sig_peptide

<222> (12)..(89)

<223>

<400> 25

tatatgaatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg 50
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
-25 -20 -15

ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
-10 -5 -1 1

tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct 146
Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
5 10 15

cac ttg tgg ggt caa tac tct cca ttc ttc tct ttg gct gac gaa tct 194
His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser
20 25 30 35

gct att tct cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa 242
Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln
40 45 50

gtt ttg tct aga cac ggt gct aga tac cca act tct tct aag tct aag 290
Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys
55 60 65

aag tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc 338
Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe
70 75 80

aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct 386
Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala
85 90 95

gac gac ttg act cca ttc ggt gaa caa caa atg gtt aac tct ggt att 434
Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile
100 105 110 115

aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc 482
Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe
120 125 130

gtt aga gct tct ggt tct gac aga gtt att gct tct gct gaa aag ttc 530
Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe
135 140 145

att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt gct aac cca 578
Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro
150 155 160

cac caa gct tct cca gtt att aac gtt att att cca gaa ggt gct ggt 626

His	Gln	Ala	Ser	Pro	Val	Ile	Asn	Val	Ile	Ile	Pro	Glu	Gly	Ala	Gly		
165						170					175						
tac	aac	aac	act	ttg	gac	cac	ggg	ttg	tgt	act	gct	ttc	gaa	gaa	tct	674	
Tyr	Asn	Asn	Thr	Leu	Asp	His	Gly	Leu	Cys	Thr	Ala	Phe	Glu	Glu	Ser		
180					185					190					195		
gaa	ttg	ggg	gac	gac	gtt	gaa	gct	aac	ttc	act	gct	gtt	ttc	gct	cca	722	
Glu	Leu	Gly	Asp	Asp	Val	Glu	Ala	Asn	Phe	Thr	Ala	Val	Phe	Ala	Pro		
				200					205					210			
cct	att	aga	gct	aga	ttg	gaa	gct	cac	ttg	cca	ggg	gtt	aac	ttg	act	770	
Pro	Ile	Arg	Ala	Arg	Leu	Glu	Ala	His	Leu	Pro	Gly	Val	Asn	Leu	Thr		
			215					220					225				
gac	gaa	gac	gtt	gtt	aac	ttg	atg	gac	atg	tgt	cca	ttc	gac	act	gtt	818	
Asp	Glu	Asp	Val	Val	Asn	Leu	Met	Asp	Met	Cys	Pro	Phe	Asp	Thr	Val		
		230					235					240					
gct	aga	act	tct	gac	gct	act	caa	ttg	tct	cca	ttc	tgt	gac	ttg	ttc	866	
Ala	Arg	Thr	Ser	Asp	Ala	Thr	Gln	Leu	Ser	Pro	Phe	Cys	Asp	Leu	Phe		
	245					250					255						
act	cac	gac	gaa	tgg	att	caa	tac	gac	tac	ttg	caa	tct	ttg	ggg	aag	914	
Thr	His	Asp	Glu	Trp	Ile	Gln	Tyr	Asp	Tyr	Leu	Gln	Ser	Leu	Gly	Lys		
260					265					270					275		
tac	tac	ggg	tac	ggg	gct	ggg	aac	cca	ttg	ggg	cca	gct	caa	ggg	gtt	962	
Tyr	Tyr	Gly	Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln	Gly	Val		
				280					285					290			
ggg	ttc	gtt	aac	gaa	ttg	att	gct	aga	ttg	act	cac	tct	cca	gtt	caa	1010	
Gly	Phe	Val	Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	His	Ser	Pro	Val	Gln		
			295					300					305				
gac	cac	act	tct	act	aac	cac	act	ttg	gac	tct	aac	cca	gct	act	ttc	1058	
Asp	His	Thr	Ser	Thr	Asn	His	Thr	Leu	Asp	Ser	Asn	Pro	Ala	Thr	Phe		
			310				315					320					
cca	ttg	aac	gct	act	ttg	tac	gct	gac	ttc	tct	cac	gac	aac	act	atg	1106	
Pro	Leu	Asn	Ala	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp	Asn	Thr	Met		
			325			330					335						
gtt	tct	att	ttc	ttc	gct	ttg	ggg	ttg	tac	aac	ggg	act	aag	cca	ttg	1154	
Val	Ser	Ile	Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Lys	Pro	Leu		
340					345					350					355		
tct	act	act	tct	gtt	gaa	tct	att	gaa	gaa	act	gac	ggg	tac	gct	gct	1202	
Ser	Thr	Thr	Ser	Val	Glu	Ser	Ile	Glu	Glu	Thr	Asp	Gly	Tyr	Ala	Ala		
				360					365					370			
tct	tgg	act	gtt	cca	ttc	gct	gct	aga	gct	tac	gtt	gaa	atg	atg	caa	1250	
Ser	Trp	Thr	Val	Pro	Phe	Ala	Ala	Arg	Ala	Tyr	Val	Glu	Met	Met	Gln		
			375					380					385				
tgt	gaa	gct	gaa	aag	gaa	cca	ttg	gtt	aga	gtt	ttg	gtt	aac	gac	aga	1298	
Cys	Glu	Ala	Glu	Lys	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn	Asp	Arg		

390	395	400	
gtt gtt cca ttg cac ggt tgt ggt gtt gac aag ttg ggt aga tgt aag			1346
Val Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys			
405	410	415	
aga gac gac ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac			1394
Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn			
420	425	430 435	
tgg gaa gaa tgt ttc gct taagaattca tata			1426
Trp Glu Glu Cys Phe Ala			
440			

<210> 26
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 26

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser	
-25	-20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp	
-10	-5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp	
10	15 20

Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser	
25	30 35

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser	
40	45 50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Ser	
55	60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys	
75	80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu	
90	95 100

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Val Arg Ala
 120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
 155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
 170 175 180

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
 185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 200 205 210

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
 215 220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
 250 255 260

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
 280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile

330

335

340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ala Ala Ser Trp Thr
 360 365 370

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
 375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
 425 430 435

Cys Phe Ala
 440

<210> 27
 <211> 437
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 27

Asn Ser His Ser Cys Asp Thr Val Asp Gly Tyr Gln Cys Pro Glu Ile
 1 5 10 15

Ser His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu
 20 25 30

Ser Ala Ile Ser Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val
 35 40 45

Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser
 50 55 60

Lys Lys Tyr Ser Ala Leu Ile Glu Arg Ile Gln Lys Asn Ala Thr Phe
65 70 75 80

Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala
85 90 95

Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile
100 105 110

Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Asn Ile Val Pro Phe
115 120 125

Val Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe
130 135 140

Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Ala His Gln Ala
145 150 155 160

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
165 170 175

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
180 185 190

Asp Asp Ala Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
195 200 205

Ala Arg Leu Glu Ala Leu Pro Gly Val Asn Leu Thr Asp Glu Asp Val
210 215 220

Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr Ser
225 230 235 240

Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr Ala Asp Glu
245 250 255

Trp Gln Tyr Asp Tyr Leu Gln Ser Leu Lys Tyr Tyr Gly Tyr Gly Ala
260 265 270

Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Asn Glu Leu Ile
275 280 285

Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr Ser Thr Asn His

290

295

300

Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr
 305 310 315 320

Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile Phe Phe Ala Leu
 325 330 335

Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr Ser Val Glu Ser
 340 345 350

Ile Glu Thr Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Ala Ala
 355 360 365

Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala Gly Gly Gly Gly Gly
 370 375 380

Glu Gly Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val
 385 390 395 400

Val Pro Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Leu
 405 410 415

Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp
 420 425 430

Ala Glu Cys Phe Ala
 435

<210> 28
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1) .. (1401)
 <223>

<220>
 <221> mat_peptide
 <222> (79) .. ()
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(78)
 <223>

<400> 28
 atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc 48
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -25 -20 -15

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -10 -5 -1 1 5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg 144
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20

ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct 192
 Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 25 30 35

cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa gtt ttg tct 240
 Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 40 45 50

aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct 288
 Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
 55 60 65 70

gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag 336
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85

tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg 384
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100

act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac 432
 Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115

aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct 480
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 120 125 130

tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt 528
 Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150

ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct 576
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
 155 160 165

tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac 624
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
 170 175 180

act ttg gac cac ggt act tgt act gct ttc gaa gac tct gaa tta ggt Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly 185 190 195	672
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg 200 205 210	720
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp 215 220 225 230	768
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235 240 245	816
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp 250 255 260	864
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly 265 270 275	912
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala 280 285 290	960
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr 295 300 305 310	1008
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn 315 320 325	1056
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile 330 335 340	1104
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr 345 350 355	1152
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr 360 365 370	1200
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala 375 380 385 390	1248
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro 395 400 405	1296

ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac 1344
 Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420

ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gct gaa 1392
 Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435

tgt ttc gct taa 1404
 Cys Phe Ala
 440

<210> 29
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 29

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20

Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 25 30 35

Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
 55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180

Thr Leu Asp His Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Gly
185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
200 205 210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
215 220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 360 365 370

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 425 430 435

Cys Phe Ala
 440

<210> 30
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> CDS
 <222> (1)..(1401)
 <223>

<220>
 <221> mat_peptide
 <222> (79)..()
 <223>

<220>
 <221> sig_peptide
 <222> (1)..(78)
 <223>

<400> 30
 atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -25 -20 -15

48

aca	tcc	ggt	acc	gcc	ttg	ggt	cct	cg	ggt	aac	tct	cac	tct	tgt	gac	96
Thr	Ser	Gly	Thr	Ala	Leu	Gly	Pro	Arg	Gly	Asn	Ser	His	Ser	Cys	Asp	
-10					-5				-1	1				5		
act	gtt	gac	ggt	ggt	tac	caa	tgt	ttc	cca	gaa	att	tct	cac	ttg	tgg	144
Thr	Val	Asp	Gly	Gly	Tyr	Gln	Cys	Phe	Pro	Glu	Ile	Ser	His	Leu	Trp	
			10					15					20			
ggt	aca	tac	tct	cca	ttc	ttc	tct	ttg	gct	gac	gaa	tct	gct	att	tct	192
Gly	Thr	Tyr	Ser	Pro	Phe	Phe	Ser	Leu	Ala	Asp	Glu	Ser	Ala	Ile	Ser	
		25					30					35				
cca	gac	gtt	cca	aag	ggt	tgt	aga	gtt	act	ttc	gtt	caa	gtt	ttg	tct	240
Pro	Asp	Val	Pro	Lys	Gly	Cys	Arg	Val	Thr	Phe	Val	Gln	Val	Leu	Ser	
	40					45					50					
aga	cac	ggt	gct	aga	tac	cca	act	tct	tct	gcg	tct	aag	gcg	tac	tct	288
Arg	His	Gly	Ala	Arg	Tyr	Pro	Thr	Ser	Ser	Ala	Ser	Lys	Ala	Tyr	Ser	
55					60					65				70		
gct	ttg	att	gaa	gct	att	caa	aag	aac	gct	act	gct	ttc	aag	ggt	aag	336
Ala	Leu	Ile	Glu	Ala	Ile	Gln	Lys	Asn	Ala	Thr	Ala	Phe	Lys	Gly	Lys	
			75					80						85		
tac	gct	ttc	ttg	aag	act	tac	aac	tac	act	ttg	ggt	gct	gac	gac	ttg	384
Tyr	Ala	Phe	Leu	Lys	Thr	Tyr	Asn	Tyr	Thr	Leu	Gly	Ala	Asp	Asp	Leu	
			90					95					100			
act	cca	ttc	ggt	gaa	caa	caa	atg	gtt	aac	tct	ggt	att	aag	ttc	tac	432
Thr	Pro	Phe	Gly	Glu	Gln	Gln	Met	Val	Asn	Ser	Gly	Ile	Lys	Phe	Tyr	
		105					110					115				
aga	aga	tac	aag	gct	ttg	gct	aga	aag	att	gtt	cca	ttc	att	aga	gct	480
Arg	Arg	Tyr	Lys	Ala	Leu	Ala	Arg	Lys	Ile	Val	Pro	Phe	Ile	Arg	Ala	
	120					125					130					
tct	ggt	tct	gac	aga	gtt	att	gct	tct	gct	gaa	aag	ttc	att	gaa	ggt	528
Ser	Gly	Ser	Asp	Arg	Val	Ile	Ala	Ser	Ala	Glu	Lys	Phe	Ile	Glu	Gly	
135					140					145				150		
ttc	caa	tct	gct	aag	ttg	gct	gac	cca	ggt	gct	aac	cca	cac	caa	gct	576
Phe	Gln	Ser	Ala	Lys	Leu	Ala	Asp	Pro	Gly	Ala	Asn	Pro	His	Gln	Ala	
			155					160						165		
tct	cca	gtt	att	aac	gtt	att	att	cca	gaa	ggt	gct	ggt	tac	aac	aac	624
Ser	Pro	Val	Ile	Asn	Val	Ile	Ile	Pro	Glu	Gly	Ala	Gly	Tyr	Asn	Asn	
		170						175					180			
act	ttg	gac	cac	ggt	ttg	tgt	act	gct	ttc	gaa	gaa	tct	gaa	ttg	ggt	672
Thr	Leu	Asp	His	Gly	Leu	Cys	Thr	Ala	Phe	Glu	Glu	Ser	Glu	Leu	Gly	
		185				</										

Ala	Arg	Leu	Glu	Ala	His	Leu	Pro	Gly	Val	Asn	Leu	Thr	Asp	Glu	Asp		
215					220					225					230		
gtt	gtt	aac	ttg	atg	gac	atg	tgt	cca	ttc	gac	act	gtt	gct	aga	act		816
Val	Val	Asn	Leu	Met	Asp	Met	Cys	Pro	Phe	Asp	Thr	Val	Ala	Arg	Thr		
				235					240					245			
tct	gac	gct	act	caa	ttg	tct	cca	ttc	tgt	gac	ttg	ttc	act	cac	gac		864
Ser	Asp	Ala	Thr	Gln	Leu	Ser	Pro	Phe	Cys	Asp	Leu	Phe	Thr	His	Asp		
			250					255					260				
gaa	tgg	att	caa	tac	gac	tac	ttg	caa	tct	ttg	ggc	aag	tac	tac	ggc		912
Glu	Trp	Ile	Gln	Tyr	Asp	Tyr	Leu	Gln	Ser	Leu	Gly	Lys	Tyr	Tyr	Gly		
		265					270					275					
tac	ggc	gct	ggc	aac	cca	ttg	ggc	cca	gct	caa	ggc	gtt	ggc	ttc	gtt		960
Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln	Gly	Val	Gly	Phe	Val		
	280					285					290						
aac	gaa	ttg	att	gct	aga	ttg	act	cac	tct	cca	gtt	caa	gac	cac	act		1008
Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	His	Ser	Pro	Val	Gln	Asp	His	Thr		
295					300					305					310		
tct	act	aac	cac	act	ttg	gac	tct	aac	cca	gct	act	ttc	cca	ttg	aac		1056
Ser	Thr	Asn	His	Thr	Leu	Asp	Ser	Asn	Pro	Ala	Thr	Phe	Pro	Leu	Asn		
				315					320					325			
gct	act	ttg	tac	gct	gac	ttc	tct	cac	gac	aac	act	atg	gtt	tct	att		1104
Ala	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp	Asn	Thr	Met	Val	Ser	Ile		
			330					335					340				
ttc	ttc	gct	ttg	ggc	ttg	tac	aac	ggc	act	aag	cca	ttg	tct	act	act		1152
Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Lys	Pro	Leu	Ser	Thr	Thr		
		345					350					355					
tct	gtt	gaa	tct	att	gaa	gaa	act	gac	ggc	tac	tct	gct	tct	tgg	act		1200
Ser	Val	Glu	Ser	Ile	Glu	Glu	Thr	Asp	Gly	Tyr	Ser	Ala	Ser	Trp	Thr		
	360					365					370						
gtt	cca	ttc	gct	gct	aga	gct	tac	gtt	gaa	atg	atg	caa	tgt	gaa	gct		1248
Val	Pro	Phe	Ala	Ala	Arg	Ala	Tyr	Val	Glu	Met	Met	Gln	Cys	Glu	Ala		
375					380					385				390			
gaa	aag	gaa	cca	ttg	gtt	aga	gtt	ttg	gtt	aac	gac	aga	gtt	gtt	cca		1296
Glu	Lys	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn	Asp	Arg	Val	Val	Pro		
				395					400					405			
ttg	cac	ggc	tgt	ggc	gtt	gac	aag	ttg	ggc	aga	tgt	aag	aga	gac	gac		1344
Leu	His	Gly	Cys	Gly	Val	Asp	Lys	Leu	Gly	Arg							

440

<210> 31
<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 31

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-10 -5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
25 30 35

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
120 125 130

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
 155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
 170 175 180

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
 185 190 195

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 200 205 210

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
 215 220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
 250 255 260

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
 280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
 330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 360 365 370

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala

25	30	35	
tcg agt aag ctt ccc aag gat tgc cgg atc acc ttg gta cag gtg cta Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu 40 45 50			240
tcg cgc cat gga gcg cgg tac cca acc agc tcc aag agc aaa aag tat Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr 55 60 65 70			288
aag aag ctt att acg gcg atc cag gcc aat gcc acc gac ttc aag ggc Lys Lys Leu Ile Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly 75 80 85			336
aag tac gcc ttt ttg aag acg tac aac tat act ctg ggt gcg gat gac Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp 90 95 100			384
ctc act ccc ttt ggg gag cag cag ctg gtg aac tcg ggc atc aag ttc Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe 105 110 115			432
tac cag agg tac aag gct ctg gcg cgc agt gtg gtg ccg ttt att cgc Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg 120 125 130			480
gcc tca ggc tcg gac cgg gtt att gct tcg gga gag aag ttc atc gag Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu 135 140 145 150			528
ggg ttc cag cag gcg aag ctg gct gat cct ggc gcg acg aac cgc gcc Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala 155 160 165			576
gct ccg gcg att agt gtg att att ccg gag agc gag acg ttc aac aat Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn 170 175 180			624
acg ctg gac cac ggt gtg tgc acg aag ttt gag gcg agt cag ctg gga Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly 185 190 195			672
gat gag gtt gcg gcc aat ttc act gcg ctc ttt gca ccc gac atc cga Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg 200 205 210			720
gct cgc ctc gag aag cat ctt cct ggc gtg acg ctg aca gac gag gac Ala Arg Leu Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp 215 220 225 230			768
gtt gtc agt cta atg gac atg tgt ccg ttt gat acg gta gcg cgc acc Val Val Ser Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235 240 245			816
agc gac gca agt cag ctg tca ccg ttc tgt caa ctc ttc act cac aat Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn 250 255 260			864

gag tgg aag aag tac gac tac ctt cag tcc ttg ggc aag tac tac ggc Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly 265 270 275	912
tac ggc gca ggc aac cct ctg gga ccg gct cag ggg ata ggg ttc acc Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr 280 285 290	960
aac gag ctg att gcc cgg ttg acg cgt tcg cca gtg cag gac cac acc Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr 295 300 305 310	1008
agc act aac tcg act cta gtc tcc aac ccg gcc acc ttc ccg ttg aac Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn 315 320 325	1056
gct acc atg tac gtc gac ttt tca cac gac aac agc atg gtt tcc atc Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile 330 335 340	1104
ttc ttt gca ttg ggc ctg tac aac ggc act gaa ccc ttg tcc cgg acc Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr 345 350 355	1152
tcg gtg gaa agc gcc aag gaa ttg gat ggg tat tct gca tcc tgg gtg Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val 360 365 370	1200
gtg cct ttc ggc gcg cga gcc tac ttc gag acg atg caa tgc aag tcg Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser 375 380 385 390	1248
gaa aag gag cct ctt gtt cgc gct ttg att aat gac cgg gtt gtg cca Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro 395 400 405	1296
ctg cat ggc tgc gat gtg gac aag ctg ggg cga tgc aag ctg aat gac Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp 410 415 420	1344
ttt gtc aag gga ttg agt tgg gcc aga tct ggg ggc aac tgg gga gag Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu 425 430 435	1392
tgc ttt agt tga Cys Phe Ser 440	1404

<210> 33
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 33

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-25 -20 -15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser Lys Ser Cys
-10 -5 -1 1 5

Asp Thr Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu
10 15 20

Trp Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Leu Ser Val
25 30 35

Ser Ser Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu
40 45 50

Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr
55 60 65 70

Lys Lys Leu Ile Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly
75 80 85

Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp
90 95 100

Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe
105 110 115

Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg
120 125 130

Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu
135 140 145 150

Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala
155 160 165

Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn
170 175 180

Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly
185 190 195

Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg
 200 205 210

Ala Arg Leu Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
 215 220 225 230

Val Val Ser Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn
 250 255 260

Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 265 270 275

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr
 280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
 295 300 305 310

Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile
 330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr
 345 350 355

Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val
 360 365 370

Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser
 375 380 385 390

Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp
 410 415 420

Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu
 425 430 435

Cys Phe Ser
 440

<210> 34
 <211> 1426
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> CDS
 <222> (12)..(1412)
 <223>

<220>
 <221> mat_peptide
 <222> (90)..()
 <223>

<220>
 <221> sig_peptide
 <222> (12)..(89)
 <223>

<400> 34
 tatatgaatt c atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg 50
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu
 -25 -20 -15
 ttc ggt tcc aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac 98
 Phe Gly Ser Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His
 -10 -5 -1 1
 tct tgt gac act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct 146
 Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser
 5 10 15
 cac ttg tgg ggt caa tac tct cca tac ttc tct ttg gaa gac gaa tct 194
 His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser
 20 25 30 35
 gct att tct cca gac gtt cca gac gac tgt aga gtt act ttc gtt caa 242
 Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln
 40 45 50
 gtt ttg tct aga cac ggt gct aga tac cca act gac tct aag ggt aag 290
 Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys
 55 60 65

aag tac tct gct ttg att gaa gct att caa aag aac gct act gct ttc Lys Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe 70 75 80	338
aag ggt aag tac gct ttc ttg aag act tac aac tac act ttg ggt gct Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala 85 90 95	386
gac gac ttg act cca ttc ggt gaa aac caa atg gtt aac tct ggt att Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile 100 105 110 115	434
aag ttc tac aga aga tac aag gct ttg gct aga aag att gtt cca ttc Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe 120 125 130	482
att aga gct tct ggt tct tct aga gtt att gct tct gct gaa aag ttc Ile Arg Ala Ser Gly Ser Ser Arg Val Ile Ala Ser Ala Glu Lys Phe 135 140 145	530
att gaa ggt ttc caa tct gct aag ttg gct gac cca ggt tct caa cca Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro 150 155 160	578
cac caa gct tct cca gtt att gac gtt att att tct gac gct tct tct His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Ser Asp Ala Ser Ser 165 170 175	626
tac aac aac act ttg gac cca ggt act tgt act gct ttc gaa gac tct Tyr Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Ala Phe Glu Asp Ser 180 185 190 195	674
gaa ttg gct gac act gtt gaa gct aac ttc act gct ttg ttc gct cca Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro 200 205 210	722
gct att aga gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr 215 220 225	770
gac act gaa gtt act tac ttg atg gac atg tgt tct ttc gaa act gtt Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe Glu Thr Val 230 235 240	818
gct aga act tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe 245 250 255	866
act cac gac gaa tgg aga cac tac gac tac ttg caa tct ttg aag aag Thr His Asp Glu Trp Arg His Tyr Asp Tyr Leu Gln Ser Leu Lys Lys 260 265 270 275	914
tac tac ggt cac ggt gct ggt aac cca ttg ggt cca act caa ggt gtt Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val 280 285 290	962
ggt ttc gct aac gaa ttg att gct aga ttg act aga tct cca gtt caa	1010

Gly	Phe	Ala	Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	Arg	Ser	Pro	Val	Gln	
			295					300					305			
gac	cac	act	tct	act	aac	cac	act	ttg	gac	tct	aac	cca	gct	act	ttc	1058
Asp	His	Thr	Ser	Thr	Asn	His	Thr	Leu	Asp	Ser	Asn	Pro	Ala	Thr	Phe	
		310					315					320				
cca	ttg	aac	gct	act	ttg	tac	gct	gac	ttc	tct	cac	gac	aac	ggg	att	1106
Pro	Leu	Asn	Ala	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp	Asn	Gly	Ile	
	325					330					335					
att	tct	att	ttc	ttc	gct	ttg	ggg	ttg	tac	aac	ggg	act	gct	cca	ttg	1154
Ile	Ser	Ile	Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Ala	Pro	Leu	
340					345					350				355		
tct	act	act	tct	gtt	gaa	tct	att	gaa	gaa	act	gac	ggg	tac	tct	tct	1202
Ser	Thr	Thr	Ser	Val	Glu	Ser	Ile	Glu	Glu	Thr	Asp	Gly	Tyr	Ser	Ser	
			360					365					370			
gct	tgg	act	gtt	cca	ttc	gct	tct	aga	gct	tac	gtt	gaa	atg	atg	caa	1250
Ala	Trp	Thr	Val	Pro	Phe	Ala	Ser	Arg	Ala	Tyr	Val	Glu	Met	Met	Gln	
		375						380					385			
tgt	caa	gct	gaa	aag	gaa	cca	ttg	gtt	aga	gtt	ttg	gtt	aac	gac	aga	1298
Cys	Gln	Ala	Glu	Lys	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn	Asp	Arg	
	390						395					400				
gtt	gtt	cca	ttg	cac	ggg	tgt	gct	gtt	gac	aag	ttg	ggg	aga	tgt	aag	1346
Val	Val	Pro	Leu	His	Gly	Cys	Ala	Val	Asp	Lys	Leu	Gly	Arg	Cys	Lys	
	405					410					415					
aga	gac	gac	ttc	gtt	gaa	ggg	ttg	tct	ttc	gct	aga	tct	ggg	ggg	aac	1394
Arg	Asp	Asp	Phe	Val	Glu	Gly	Leu	Ser	Phe	Ala	Arg	Ser	Gly	Gly	Asn	
420					425					430				435		
tgg	gct	gaa	tgt	ttc	gct	taagaattca tata										1426
Trp	Ala	Glu	Cys	Phe	Ala											
					440											

<210> 35
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 35

Met	Gly	Val	Phe	Val	Val	Leu	Leu	Ser	Ile	Ala	Thr	Leu	Phe	Gly	Ser
-25						-20					-15				

Thr	Ser	Gly	Thr	Ala	Leu	Gly	Pro	Arg	Gly	Asn	Ser	His	Ser	Cys	Asp
-10					-5				-1	1				5	

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20

Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu Asp Glu Ser Ala Ile Ser
 25 30 35

Pro Asp Val Pro Asp Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 40 45 50

Arg His Gly Ala Arg Tyr Pro Thr Asp Ser Lys Gly Lys Lys Tyr Ser
 55 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 105 110 115

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 120 125 130

Ser Gly Ser Ser Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 135 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
 155 160 165

Ser Pro Val Ile Asp Val Ile Ile Ser Asp Ala Ser Ser Tyr Asn Asn
 170 175 180

Thr Leu Asp Pro Gly Thr Cys Thr Ala Phe Glu Asp Ser Glu Leu Ala
 185 190 195

Asp Thr Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
 200 205 210

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Thr Glu
 215 220 225 230

Val Thr Tyr Leu Met Asp Met Cys Ser Phe Glu Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
250 255 260

Glu Trp Arg His Tyr Asp Tyr Leu Gln Ser Leu Lys Lys Tyr Tyr Gly
265 270 275

His Gly Ala Gly Asn Pro Leu Gly Pro Thr Gln Gly Val Gly Phe Ala
280 285 290

Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr
295 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Gly Ile Ile Ser Ile
330 335 340

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Ala Pro Leu Ser Thr Thr
345 350 355

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ser Ala Trp Thr
360 365 370

Val Pro Phe Ala Ser Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
375 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
425 430 435

Cys Phe Ala
440

<210> 36

<211> 467
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 36

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
1 5 10 15

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
20 25 30

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser Ser Asn Trp
35 40 45

Ser Pro Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
50 55 60

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Gln
65 70 75 80

Arg His Gly Ala Arg Phe Pro Thr Ser Gly Ala Ala Thr Arg Ile Ser
85 90 95

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
100 105 110

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
115 120 125

Val Pro Phe Gly Ala Asn Gln Ser Ser Gln Ala Gly Ile Lys Phe Tyr
130 135 140

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
145 150 155 160

Ser Gly Ser Asp Arg Val Ile Asp Ser Ala Thr Asn Trp Ile Glu Gly
165 170 175

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
180 185 190

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
195 200 205

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Glu Leu Gly
210 215 220

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
225 230 235 240

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
245 250 255

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
260 265 270

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
275 280 285

Glu Trp Ile Gln Tyr Asp Tyr Leu Gly Asp Leu Asp Lys Tyr Tyr Gly
290 295 300

Thr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
305 310 315 320

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
325 330 335

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
340 345 350

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ala Ile
355 360 365

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
370 375 380

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Leu
385 390 395 400

Val Pro Phe Ser Ala Arg Met Tyr Val Glu Met Met Gln Cys Glu Ala
405 410 415

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro

420

425

430

Leu His Gly Cys Gly Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 435 440 445

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
 450 455 460

Cys Phe Ala
 465

<210> 37
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 37
 tatatgaatt catgggcgtg ttcgtc

26

<210> 38
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 38
 tgaaaagttc attgaaggtt tc

22

<210> 39
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 39
 tcttcgaaag cagtacacaa ac

22

<210> 40
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Primer

<400> 40

tatatgaatt cttaagcgaa ac

22

<210> 41

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 41

cacttgtaggg gtacctactc tccatacttc tc

32

<210> 42

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 42

ggtcaatact ctccattctt ctctttggaa g

31

<210> 43

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 43

catacttctc tttggcagac gaatctgc

28

<210> 44

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 44

ctccagacgt cccaaaggac thtagagtta c

31

<210> 45

<211> 31

<212> DNA

<213> Artificial Sequence
 <220>
 <223> Primer
 <400> 45
 ctccagacgt cccagacggc tgtagagtta c 31

<210> 46
 <211> 36
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 46
 gatacccaac ttctttctgcg tctaaggctt actctg 36

<210> 47
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 47
 cttctaagtc taagaagtac tctgctttg 29

<210> 48
 <211> 41
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 48
 gcttactctg ctttgattga acggattcaa aagaacgcta c 41

<210> 49
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 49
 ccattcgggtg aacagcaa at ggттаactc 29

<210> 50
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 50
gatacaaggc tctcgcgaga aacattgttc

30

<210> 51
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 51
gattgttcca ttcgtgcgcg cttctggttc

30

<210> 52
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 52
ctccagttat taacgtgatc attccagaag g

31

<210> 53
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 53
ggctgaccca ggggcccaac cacaccaagc

30

<210> 54
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 54

cactttggac catggtcttt gtactgcttt cg

32

<210> 55
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 55
gctttcgaag actctaccct aggtgacgac gttg

34

<210> 56
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 56
ggtgacgacg ctgaagctaa cttcac

26

<210> 57
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 57
ctaacttcac cgcggtgttc gctccag

27

<210> 58
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 58
gctttgttcg ctccacctat tagagctaga ttgg

34

<210> 59
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer
 <400> 59
 gccaggtggt aacttgactg acgaag 26
 <210> 60
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 60
 gacgaagacg tcgttaactt gatggac 27
 <210> 61
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 61
 gtccattcga cactgtcgtc agaacttc 28
 <210> 62
 <211> 26
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 62
 ctgacgtac tcagctgtct ccattc 26
 <210> 63
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 63
 gtctccattc tgtgatttgc tcactcac 28
 <210> 64
 <211> 26
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> Primer
 <400> 64
 gctttgttca ccgcggacga atggag 26
 <210> 65
 <211> 27
 <212> DNA
 <213> Primer
 <400> 65
 cacgacgaat ggatccaata cgactac 27
 <210> 66
 <211> 27
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 66
 gacgaatgga gagcgtacga ctacttg 27
 <210> 67
 <211> 29
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 67
 ggtgttggtt tcgttaacga attgattgc 29
 <210> 68
 <211> 28
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Primer
 <400> 68
 gctagattga ctactctcc agttcaag 28
 <210> 69
 <211> 32
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 69

ctcacgacaa cactatgata tctatatttct tc

32

<210> 70

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 70

cgacaactcc atggtttcta ttttcttcgc

30

<210> 71

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 71

gtacaacggt accaagccat tgtctac

27

<210> 72

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 72

ctgacggtta cgctgcttct tggac

25

<210> 73

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 73

ctgttcatt cgctgctaga gcttac

26

<210> 74
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 74
 gatgcaatgt gaagctgaaa aggaacc 27

 <210> 75
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 75
 cacggttgtg gtgtcgacaa gttggg 26

 <210> 76
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 76
 gatctggtgg caattgggag gaatgtttcg 30

 <210> 77
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 77
 cacgtactcg ccatactttt cgctcgag 28

 <210> 78
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer

 <400> 78

ccatactttt cgctcgcgga cgagctgtcc gtg

33

<210> 79

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 79

gtataagaag cttattacgg cgatccaggc c

31

<210> 80

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 80

cttcaagggc aagtacgcct ttttgaagac g

31

<210> 81

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 81

catccgagct cgcctcgaga agcatcttc

29

<210> 82

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 82

ctaattgatg tgtccgtttg atacggtag

29

<210> 83

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 83

gtggaagaag tacgactacc ttcagtc

27

<210> 84

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 84

gcccgggtga cgcattcgcc agtgcagg

28

<210> 85

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 85

cacacgacaa caccatggtt tccatcttc

29

<210> 86

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 86

gtggtgcctt tcgccgcgcg agcctacttc

30

<210> 87

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 87

tatatcatga gcgtgttcgt cgtgctactg ttc

33

<210> 88

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 88

acccgactta caaagcgaat tctatagata tat

33

<210> 89

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 89

acccttctta caaagcgaat tctatagata tat

33

<210> 90

<211> 1404

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<220>

<221> CDS

<222> (1)..(1401)

<223>

<220>

<221> sig_peptide

<222> (1)..(69)

<223>

<220>

<221> mat_peptide

<222> (70)..()

<223>

<400> 90

atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

48

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

96

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

144

ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser 30 35 40	192
cca gac gtc cca aag gac tgt aga gtt act ttc gtt caa gtt ttg tct Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser 45 50 55	240
aga cac ggt gct aga tac cca act tct tct aag tct aag gct tac tct Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser 60 65 70	288
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys 75 80 85	336
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu 90 95 100 105	384
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr 110 115 120	432
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala 125 130 135	480
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly 140 145 150	528
ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala 155 160 165	576
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn 170 175 180 185	624
act ttg gac cat ggt ctt tgt act gct ttc gaa gac tct acc cta ggt Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly 190 195 200	672
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg 205 210 215	720
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp 220 225 230	768
ggt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235 240 245	816
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac	864

Ser 250	Asp	Ala	Thr	Glu	Leu	Ser 255	Pro	Phe	Cys	Ala 260	Leu	Phe	Thr	His	Asp 265	
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt 912																
Glu	Trp	Ile	Gln	Tyr	Asp	Tyr	Leu	Gln	Ser	Leu	Gly	Lys	Tyr	Tyr	Gly	
			270						275					280		
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct 960																
Tyr	Gly	Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln	Gly	Val	Gly	Phe	Ala	
			285						290					295		
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act 1008																
Asn	Glu	Leu	Ile	Ala	Arg	Leu	Thr	His	Ser	Pro	Val	Gln	Asp	His	Thr	
		300						305					310			
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac 1056																
Ser	Thr	Asn	His	Thr	Leu	Asp	Ser	Asn	Pro	Ala	Thr	Phe	Pro	Leu	Asn	
		315				320						325				
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att 1104																
Ala	Thr	Leu	Tyr	Ala	Asp	Phe	Ser	His	Asp	Asn	Thr	Met	Ile	Ser	Ile	
		330			335					340				345		
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act 1152																
Phe	Phe	Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Lys	Pro	Leu	Ser	Thr	Thr	
			350					355						360		
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act 1200																
Ser	Val	Glu	Ser	Ile	Glu	Glu	Thr	Asp	Gly	Tyr	Ser	Ala	Ser	Trp	Thr	
			365					370					375			
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct 1248																
Val	Pro	Phe	Ala	Ala	Arg	Ala	Tyr	Val	Glu	Met	Met	Gln	Cys	Gln	Ala	
			380				385					390				
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca 1296																
Glu	Lys	Glu	Pro	Leu	Val	Arg	Val	Leu	Val	Asn	Asp	Arg	Val	Val	Pro	
		395				400					405					
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac 1344																
Leu	His	Gly	Cys	Ala	Val	Asp	Lys	Leu	Gly	Arg	Cys	Lys	Arg	Asp	Asp	
		410			415				420					425		
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gct gaa 1392																
Phe	Val	Glu	Gly	Leu	Ser	Phe	Ala	Arg	Ser	Gly	Gly	Asn	Trp	Ala	Glu	
			430					435					440			
tgt ttc gct taa 1404																
Cys	Phe	Ala														

<210> 91
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Primer
 <400> 91
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -20 -15 -10
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -5 -1 1 5
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20 25
 Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 30 35 40
 Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 45 50 55
 Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
 60 65 70
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100 105
 Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 110 115 120
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 125 130 135
 Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 140 145 150
 Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
 155 160 165
 Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
 170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
 190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
 205 210 215

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
 220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
 285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
 330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp

410

415

420

425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 430 435 440

Cys Phe Ala

<210> 92
 <211> 1404
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic

<220>
 <221> sig_peptide
 <222> (1)..(69)
 <223>

<220>
 <221> CDS
 <222> (1)..(1401)
 <223>

<220>
 <221> mat_peptide
 <222> (70)..()
 <223>

<400> 92
 atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc 48
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -20 -15 -10
 aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -5 -1 1 5
 act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg 144
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20 25
 ggt acc tac tct cca tac ttc tct ttg gca gac gaa tct gct att tct 192
 Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 30 35 40
 cca gac gtc cca aag gac tgt aga gtt act ttc gtt caa gtt ttg tct 240
 Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
 45 50 55
 aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct 288
 Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser

60	65	70	
gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys 75 80 85	336		
tac gct ttc ttg aag act tac aac tac act ttg ggt gct gac gac ttg Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu 90 95 100 105	384		
act cca ttc ggt gaa aac caa atg gtt aac tct ggt att aag ttc tac Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr 110 115 120	432		
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala 125 130 135	480		
tct ggt tct gac aga gtt att gct tct gct gaa aag ttc att gaa ggt Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly 140 145 150	528		
ttc caa tct gct aag ttg gct gac cca ggt tct caa cca cac caa gct Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala 155 160 165	576		
tct cca gtt att aac gtg atc att cca gaa gga tcc ggt tac aac aac Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn 170 175 180 185	624		
act ttg gac cat ggt ctt tgt act gct ttc gaa gac tct acc cta ggt Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly 190 195 200	672		
gac gac gtt gaa gct aac ttc act gct ttg ttc gct cca gct att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg 205 210 215	720		
gct aga ttg gaa gct gac ttg cca ggt gtt act ttg act gac gaa gac Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp 220 225 230	768		
gtt gtt tac ttg atg gac atg tgt cca ttc gac act gtc gct aga act Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235 240 245	816		
tct gac gct act gaa ttg tct cca ttc tgt gct ttg ttc act cac gac Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp 250 255 260 265	864		
gaa tgg atc caa tac gac tac ttg caa agc ttg ggt aag tac tac ggt Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly 270 275 280	912		
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gct Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala 285 290 295	960		

aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr 300 305 310	1008
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn 315 320 325	1056
gct act ttg tac gct gac ttc tct cac gac aac act atg ata tct att Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile 330 335 340 345	1104
ttc ttc gct ttg ggt ttg tac aac ggt acc aag cca ttg tct act act Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr 350 355 360	1152
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr 365 370 375	1200
gtt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt caa gct Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala 380 385 390	1248
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro 395 400 405	1296
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp 410 415 420 425	1344
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gct gaa Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu 430 435 440	1392
tgt ttc gct taa Cys Phe Ala	1404

<210> 93
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 93

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp

-5

-1 1

5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Tyr Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30 35 40

Pro Asp Val Pro Lys Asp Cys Arg Val Thr Phe Val Gln Val Leu Ser
45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
75 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100 105

Thr Pro Phe Gly Glu Asn Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ser Gln Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ser Gly Tyr Asn Asn
170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Asp Ser Thr Leu Gly
190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala Ile Arg
205 210 215

Ala Arg Leu Glu Ala Asp Leu Pro Gly Val Thr Leu Thr Asp Glu Asp
220 225 230

Val Val Tyr Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys Ala Leu Phe Thr His Asp
 250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
 270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Ala
 285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
 300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
 315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Ile Ser Ile
 330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
 350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
 365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Gln Ala
 380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
 395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
 410 415 420 425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Ala Glu
 430 435 440

Cys Phe Ala

```

<210> 94
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>
<221> sig_peptide
<222> (1)..(69)
<223>

<220>
<221> CDS
<222> (1)..(1401)
<223>

<220>
<221> mat_peptide
<222> (70)..()
<223>

<400> 94
atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc      48
Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
      -20                      -15                      -10

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac      96
Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
      -5                      -1 1                      5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg      144
Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10                      15                      20                      25

ggt aca tac tct cca ttc ttc tct ttg gct gac gaa tct gct att tct      192
Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
      30                      35                      40

cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa gtt ttg tct      240
Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
      45                      50                      55

aga cac ggt gct aga tac cca act tct tct aag tct aag gct tac tct      288
Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
      60                      65                      70

gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag      336
Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
      75                      80                      85

tac gct ttc ttg aag act tac aat tac act ttg ggt gct gac gac ttg      384
Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90                      95                      100                      105

```

act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac	432
Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr	
110 115 120	
aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct	480
Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala	
125 130 135	
tct ggt tct gac aga gtt att gct tct gcc gaa aag ttc att gaa ggt	528
Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly	
140 145 150	
ttc caa tct gct aag ttg gct gac cca ggt gct aac cca cac caa gct	576
Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala	
155 160 165	
tct cca gtt att aac gtt att att cca gaa ggt gct ggt tac aac aac	624
Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn	
170 175 180 185	
act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct acc cta ggt	672
Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly	
190 195 200	
gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca cca att aga	720
Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg	
205 210 215	
gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act gac gaa gac	768
Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp	
220 225 230	
gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt gct aga act	816
Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr	
235 240 245	
tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc act cac gac	864
Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp	
250 255 260 265	
gaa tgg att caa tac gac tac ttg caa tct ttg ggt aag tac tac ggt	912
Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly	
270 275 280	
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gtt	960
Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val	
285 290 295	
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act	1008
Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr	
300 305 310	
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac	1056
Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn	
315 320 325	
gct act ttg tac gct gac ttc tct cac gac aac act atg gtt tct att	1104

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
 45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Ala Tyr Ser
 60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100 105

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
 140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
 155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
 170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly
 190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
 205 210 215

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
 220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
 235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
 250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420 425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
430 435 440

Cys Phe Ala

<210> 96
<211> 1404
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<220>

<221> sig_peptide
 <222> (1)..(69)
 <223>

<220>
 <221> CDS
 <222> (1)..(1401)
 <223>

<220>
 <221> mat_peptide
 <222> (70)..()
 <223>

<400> 96

atg ggc gtg ttc gtc gtg cta ctg tcc att gcc acc ttg ttc ggt tcc 48
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
 -20 -15 -10

aca tcc ggt acc gcc ttg ggt cct cgt ggt aat tct cac tct tgt gac 96
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
 -5 -1 1 5

act gtt gac ggt ggt tac caa tgt ttc cca gaa att tct cac ttg tgg 144
 Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
 10 15 20 25

ggt aca tac tct cca ttc ttc tct ttg gct gac gaa tct gct att tct 192
 Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
 30 35 40

cca gac gtt cca aag ggt tgt aga gtt act ttc gtt caa gtt ttg tct 240
 Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
 45 50 55

aga cac ggt gct aga tac cca act tct tct gcg tct aag gct tac tct 288
 Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
 60 65 70

gct ttg att gaa gct att caa aag aac gct act gct ttc aag ggt aag 336
 Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys
 75 80 85

tac gct ttc ttg aag act tac aat tac act ttg ggt gct gac gac ttg 384
 Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
 90 95 100 105

act cca ttc ggt gaa caa caa atg gtt aac tct ggt att aag ttc tac 432
 Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
 110 115 120

aga aga tac aag gct ttg gct aga aag att gtt cca ttc att aga gct 480
 Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
 125 130 135

tct ggt tct gac aga gtt att gct tct gcc gaa aag ttc att gaa ggt 528
 Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly

140	145	150	
ttc caa tct gct aag ttg gct gac cca ggt gct aac cca cac caa gct Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala 155 160 165			576
tct cca gtt att aac gtt att att cca gaa ggt gct ggt tac aac aac Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn 170 175 180 185			624
act ttg gac cac ggt ttg tgt act gct ttc gaa gaa tct acc cta ggt Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly 190 195 200			672
gac gac gtt gaa gct aac ttc act gct gtt ttc gct cca cca att aga Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg 205 210 215			720
gct aga ttg gaa gct cac ttg cca ggt gtt aac ttg act gac gaa gac Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp 220 225 230			768
gtt gtt aac ttg atg gac atg tgt cca ttc gac act gtt gct aga act Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr 235 240 245			816
tct gac gct act caa ttg tct cca ttc tgt gac ttg ttc act cac gac Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp 250 255 260 265			864
gaa tgg att caa tac gac tac ttg cca tct ttg ggt aag tac tac ggt Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly 270 275 280			912
tac ggt gct ggt aac cca ttg ggt cca gct caa ggt gtt ggt ttc gtt Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val 285 290 295			960
aac gaa ttg att gct aga ttg act cac tct cca gtt caa gac cac act Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr 300 305 310			1008
tct act aac cac act ttg gac tct aac cca gct act ttc cca ttg aac Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn 315 320 325			1056
gct act ttg tac gct gac ttc tct cac gac aac act atg gtt tct att Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile 330 335 340 345			1104
ttc ttc gct ttg ggt ttg tac aac ggt act aag cca ttg tct act act Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr 350 355 360			1152
tct gtt gaa tct att gaa gaa act gac ggt tac tct gct tct tgg act Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr 365 370 375			1200

ggt cca ttc gct gct aga gct tac gtt gaa atg atg caa tgt gaa gct	1248
Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala	
380 385 390	
gaa aag gaa cca ttg gtt aga gtt ttg gtt aac gac aga gtt gtt cca	1296
Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro	
395 400 405	
ttg cac ggt tgt gct gtt gac aag ttg ggt aga tgt aag aga gac gac	1344
Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp	
410 415 420 425	
ttc gtt gaa ggt ttg tct ttc gct aga tct ggt ggt aac tgg gaa gaa	1392
Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu	
430 435 440	
tgt ttc gct taa	1404
Cys Phe Ala	

<210> 97
 <211> 467
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic

<400> 97

Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser
-20 -15 -10

Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn Ser His Ser Cys Asp
-5 -1 1 5

Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro Glu Ile Ser His Leu Trp
10 15 20 25

Gly Thr Tyr Ser Pro Phe Phe Ser Leu Ala Asp Glu Ser Ala Ile Ser
30 35 40

Pro Asp Val Pro Lys Gly Cys Arg Val Thr Phe Val Gln Val Leu Ser
45 50 55

Arg His Gly Ala Arg Tyr Pro Thr Ser Ser Ala Ser Lys Ala Tyr Ser
60 65 70

Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala Thr Ala Phe Lys Gly Lys

75

80

85

Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu
90 95 100 105

Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile Lys Phe Tyr
110 115 120

Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile Val Pro Phe Ile Arg Ala
125 130 135

Ser Gly Ser Asp Arg Val Ile Ala Ser Ala Glu Lys Phe Ile Glu Gly
140 145 150

Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly Ala Asn Pro His Gln Ala
155 160 165

Ser Pro Val Ile Asn Val Ile Ile Pro Glu Gly Ala Gly Tyr Asn Asn
170 175 180 185

Thr Leu Asp His Gly Leu Cys Thr Ala Phe Glu Glu Ser Thr Leu Gly
190 195 200

Asp Asp Val Glu Ala Asn Phe Thr Ala Val Phe Ala Pro Pro Ile Arg
205 210 215

Ala Arg Leu Glu Ala His Leu Pro Gly Val Asn Leu Thr Asp Glu Asp
220 225 230

Val Val Asn Leu Met Asp Met Cys Pro Phe Asp Thr Val Ala Arg Thr
235 240 245

Ser Asp Ala Thr Gln Leu Ser Pro Phe Cys Asp Leu Phe Thr His Asp
250 255 260 265

Glu Trp Ile Gln Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly
270 275 280

Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val
285 290 295

Asn Glu Leu Ile Ala Arg Leu Thr His Ser Pro Val Gln Asp His Thr
300 305 310

Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn
315 320 325

Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Asn Thr Met Val Ser Ile
330 335 340 345

Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Thr Thr
350 355 360

Ser Val Glu Ser Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ser Trp Thr
365 370 375

Val Pro Phe Ala Ala Arg Ala Tyr Val Glu Met Met Gln Cys Glu Ala
380 385 390

Glu Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Val Pro
395 400 405

Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Arg Asp Asp
410 415 420 425

Phe Val Glu Gly Leu Ser Phe Ala Arg Ser Gly Gly Asn Trp Glu Glu
430 435 440

Cys Phe Ala

<210> 98
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 98

Asn Ser His Ser Cys Asp Thr Val Asp Gly Gly Tyr Gln Cys Phe Pro
1 5 10 15

Glu Ile Ser His Leu Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Leu Glu
20 25 30

Asp Glu Ser Ala Ile Ser Pro Asp Val Pro Asp Asp Cys Arg Val Thr

35

40

45

Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ser Ser
50 55 60

Lys Ser Lys Ala Tyr Ser Ala Leu Ile Glu Ala Ile Gln Lys Asn Ala
65 70 75 80

Thr Ala Phe Lys Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Thr
85 90 95

Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Asn Gln Met Val Asn
100 105 110

Ser Gly Ile Lys Phe Tyr Arg Arg Tyr Lys Ala Leu Ala Arg Lys Ile
115 120 125

Val Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Ala
130 135 140

Glu Lys Phe Ile Glu Gly Phe Gln Ser Ala Lys Leu Ala Asp Pro Gly
145 150 155 160

Ser Gln Pro His Gln Ala Ser Pro Val Ile Asp Val Ile Ile Pro Glu
165 170 175

Gly Ser Gly Tyr Asn Asn Thr Leu Asp His Gly Thr Cys Thr Ala Phe
180 185 190

Glu Asp Ser Glu Leu Gly Asp Asp Val Glu Ala Asn Phe Thr Ala Leu
195 200 205

Phe Ala Pro Ala Ile Arg Ala Arg Leu Glu Ala Asp Leu Pro Gly Val
210 215 220

Thr Leu Thr Asp Glu Asp Val Val Tyr Leu Met Asp Met Cys Pro Phe
225 230 235 240

Glu Thr Val Ala Arg Thr Ser Asp Ala Thr Glu Leu Ser Pro Phe Cys
245 250 255

Ala Leu Phe Thr His Asp Glu Trp Arg Gln Tyr Asp Tyr Leu Gln Ser
260 265 270

Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala
 275 280 285

Gln Gly Val Gly Phe Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
 290 295 300

Pro Val Gln Asp His Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro
 305 310 315 320

Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 325 330 335

Asn Ser Met Ile Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 340 345 350

Ala Pro Leu Ser Thr Thr Ser Val Glu Ser Ile Glu Glu Thr Asp Gly
 355 360 365

Tyr Ser Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Val Glu
 370 375 380

Met Met Gln Cys Gln Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
 385 390 395 400

Asn Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly
 405 410 415

Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ser
 420 425 430

Gly Gly Asn Trp Ala Glu Cys Phe Ala
 435 440